RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/519,335_
Source: _Pu/io_
Date Processed by STIC: _10/28/05_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 10/28/2005
PATENT APPLICATION: US/10/519,335   TIME: 12:21:46

Input Set : N:\RJAVED\10519335.txt
Output Set: N:\CRF4\10282005\J519335.raw

```
 3 <110> APPLICANT: Cavarec, Laurent
 4        Chumakov, Ilya
 5        Destenaves, Benoit
 6        Gonthier, Catherine
 7        Elias, Isabelle
 9 <120> TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES
IN THE
10        TREATMENT OF MENTAL DISORDERS
12 <130> FILE REFERENCE: G-194US03PCT
14 <140> CURRENT APPLICATION NUMBER: US 10/519,335
15 <141> CURRENT FILING DATE: 2004-12-22
17 <150> PRIOR APPLICATION NUMBER: US 60/391,359
18 <151> PRIOR FILING DATE: 2002-06-25
20 <160> NUMBER OF SEQ ID NOS: 47
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1932
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1932)
33 <400> SEQUENCE: 1
34 atg gtg cag aag tcg cgc aac ggc ggc gta tac ccc ggc ccg agc ggg      48
35 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
36 1               5                   10                  15
38 gag aag aag ctg aag gtg ggc ttc gtg ggg ctg gac ccc ggc gcg ccc      96
39 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
40              20                  25                  30
42 gac tcc acc cgg gac ggg gcg ctg ctg atc gcc ggc tcc gag gcc ccc     144
43 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
44          35                  40                  45
46 aag cgc ggc agc atc ctc agc aaa cct cgc gcg ggc ggc gcg ggc gcc     192
47 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
48      50                  55                  60
50 ggg aag ccc ccc aag cgc aac gcc ttc tac cgc aag ctg cag aat ttc     240
51 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
52 65                  70                  75                  80
54 ctc tac aac gtg ctg gag cgg ccg cgc ggc tgg gcg ttc atc tac cac     288
55 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
56              85                  90                  95
58 gcc tac gtg ttc ctc ctg gtt ttc tcc tgc ctc gtg ctg tct gtg ttt     336
59 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
60             100                 105                 110
```

```
62 tcc acc atc aag gag tat gag aag agc tcg gag ggg gcc ctc tac atc        384
63 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
64         115             120             125
66 ctg gaa atc gtg act atc gtg gtg ttt ggc gtg gag tac ttc gtg cgg        432
67 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
68         130             135             140
70 atc tgg gcc gca ggc tgc tgc tgc cgg tac cgt ggc tgg agg ggg cgg        480
71 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
72 145             150             155             160
74 ctc aag ttt gcc cgg aaa ccg ttc tgt gtg att gac atc atg gtg ctc        528
75 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
76             165             170             175
78 atc gcc tcc att gcg gtg ctg gcc gcc ggc tcc cag ggc aac gtc ttt        576
79 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
80             180             185             190
82 gcc aca tct gcg ctc cgg agc ctg cgc ttc ctg cag att ctg cgg atg        624
83 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
84             195             200             205
86 atc cgc atg gac cgg cgg gga ggc acc tgg aag ctg ctg ggc tct gtg        672
87 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
88         210             215             220
90 gtc tat gcc cac agc aag gag ctg gtc act gcc tgg tac atc ggc ttc        720
91 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
92 225             230             235             240
94 ctt tgt ctc atc ctg gcc tcg ttc ctg gtg tac ttg gca gag aag ggg        768
95 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
96             245             250             255
98 gag aac gac cac ttt gac acc tac gcg gat gca ctc tgg tgg ggc ctg        816
99 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
100             260             265             270
102 atc acg ctg acc acc att ggc tac ggg gac aag tac ccc cag acc tgg        864
103 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
104         275             280             285
106 aac ggc agg ctc ctt gcg gca acc ttc acc ctc atc ggt gtc tcc ttc        912
107 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
108         290             295             300
110 ttc gcg ctg cct gca ggc atc ttg ggg tct ggg ttt gcc ctg aag gtt        960
111 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
112 305             310             315             320
114 cag gag cag cac agg cag aag cac ttt gag aag agg cgg aac ccg gca       1008
115 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
116             325             330             335
118 gca ggc ctg atc cag tcg gcc tgg aga ttc tac gcc acc aac ctc tcg       1056
119 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
120             340             345             350
122 cgc aca gac ctg cac tcc acg tgg cag tac tac gag cga acg gtc acc       1104
123 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
124             355             360             365
126 gtg ccc atg tac agt tcg caa act caa acc tac ggg gcc tcc aga ctt       1152
```

```
127 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
128     370             375             380
130 atc ccc ccg ctg aac cag ctg gag ctg ctg agg aac ctc aag agt aaa     1200
131 Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
132 385             390             395             400
134 tct gga ctc gct ttc agg aag gac ccc ccg ccg gag ccg tct cca agt     1248
135 Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Glu Pro Ser Pro Ser
136             405             410             415
138 aaa ggc agc ccg tgc aga ggg ccc ctg tgt gga tgc tgc ccc gga cgc     1296
139 Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
140             420             425             430
142 tct agc cag aag gtc agt ttg aaa gat cgt gtc ttc tcc agc ccc cga     1344
143 Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
144             435             440             445
146 ggc gtg gct gcc aag ggg aag ggg tcc ccg cag gcc cag act gtg agg     1392
147 Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
148     450             455             460
150 cgg tca ccc agc gcc gac cag agc ctc gag gac agc ccc agc aag gtg     1440
151 Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
152 465             470             475             480
154 ccc aag agc tgg agc ttc ggg gac cgc agc cgg gca cgc cag gct ttc     1488
155 Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
156             485             490             495
158 cgc atc aag ggt gcc gcg tca cgg cag aac tca gaa gaa gca agc ctc     1536
159 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
160             500             505             510
162 ccc gga gag gac att gtg gat gac aag agc tgc ccc tgc gag ttt gtg     1584
163 Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
164             515             520             525
166 acc gag gac ctg acc ccg ggc ctc aaa gtc agc atc aga gcc gtg tgt     1632
167 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
168     530             535             540
170 gtc atg cgg ttc ctg gtg tcc aag cgg aag ttc aag gag agc ctg cgg     1680
171 Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
172 545             550             555             560
174 ccc tac gac gtg atg gac gtc atc gag cag tac tca gcc ggc cac ctg     1728
175 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
176             565             570             575
178 gac atg ctg tcc cga att aag agc ctg cag tcc agg caa gag ccc cgc     1776
179 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
180             580             585             590
182 ctg cct gtc cag cag ggg aca aga acg ggg tgg gct tct ggg aca aag     1824
183 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
184             595             600             605
186 ccc act gtg gcc cat ggt ggg agt gca ggg ggt gtg tgg gcg ggg cct     1872
187 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
188     610             615             620
190 cct ccc cac cca cgt cgg cct ctg tca gct tct gtt gtg tct tca caa     1920
191 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
```

```
192 625                 630               635               640
194 agt ctg ttt taa                                                    1932
195 Ser Leu Phe
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 643
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 2
206 Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
207 1               5                   10                  15
210 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
211             20                  25                  30
214 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
215         35                  40                  45
218 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
219     50                  55                  60
222 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
223 65                  70                  75                  80
226 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
227                 85                  90                  95
230 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
231             100                 105                 110
234 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
235             115                 120                 125
238 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
239     130                 135                 140
242 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
243 145                 150                 155                 160
246 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
247             165                 170                 175
250 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
251             180                 185                 190
254 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
255         195                 200                 205
258 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
259     210                 215                 220
262 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
263 225                 230                 235                 240
266 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
267             245                 250                 255
270 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
271             260                 265                 270
274 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275         275                 280                 285
278 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
279     290                 295                 300
282 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
283 305                 310                 315                 320
286 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
```

RAW SEQUENCE LISTING   DATE: 10/28/2005
PATENT APPLICATION: US/10/519,335   TIME: 12:21:46

Input Set : N:\RJAVED\10519335.txt
Output Set: N:\CRF4\10282005\J519335.raw

```
287                   325                   330                   335
290 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
291               340                   345                   350
294 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
295           355                   360                   365
298 Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
299       370                   375                   380
302 Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
303 385                   390                   395                   400
306 Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Glu Pro Ser Pro Ser
307             405                   410                   415
310 Lys Gly Ser Pro Cys Arg Gly Pro Leu Cys Gly Cys Cys Pro Gly Arg
311             420                   425                   430
314 Ser Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg
315           435                   440                   445
318 Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg
319       450                   455                   460
322 Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val
323 465                   470                   475                   480
326 Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe
327             485                   490                   495
330 Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu
331             500                   505                   510
334 Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val
335           515                   520                   525
338 Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys
339       530                   535                   540
342 Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg
343 545                   550                   555                   560
346 Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
347             565                   570                   575
350 Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Gln Glu Pro Arg
351             580                   585                   590
354 Leu Pro Val Gln Gln Gly Thr Arg Thr Gly Trp Ala Ser Gly Thr Lys
355       595                   600                   605
358 Pro Thr Val Ala His Gly Gly Ser Ala Gly Gly Val Trp Ala Gly Pro
359       610                   615                   620
362 Pro Pro His Pro Arg Arg Pro Leu Ser Ala Ser Val Val Ser Ser Gln
363 625                   630                   635                   640
366 Ser Leu Phe
370 <210> SEQ ID NO: 3
371 <211> LENGTH: 1878
372 <212> TYPE: DNA
373 <213> ORGANISM: Homo sapiens
375 <220> FEATURE:
376 <221> NAME/KEY: CDS
377 <222> LOCATION: (1)..(1878)
379 <400> SEQUENCE: 3
380 atg gtg cag aag tcg cgc aac ggc ggc gta tac ccc ggc ccg agc ggg        48
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/28/2005
PATENT APPLICATION: US/10/519,335   TIME: 12:21:47

Input Set : N:\RJAVED\10519335.txt
Output Set: N:\CRF4\10282005\J519335.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:37;  N Pos.  10,5363,8080,10296,14528,15336,15457,16288,16306,16307
Seq#:37;  N Pos.  16316,16397,56012,57662
Seq#:37;  N Pos.  60402,61110,98207,98208,98209,98210,98211,99743,108055
Seq#:37;  N Pos.  109094,109125
Seq#:37;  N Pos.  118900,119024,119025,119026,119027,119028,119029,119030
Seq#:37;  N Pos.  119031,119032,119033,119034,119035,119036,119037,119038
Seq#:37;  N Pos.  119039,119040,119041,119042,119043,119044,119045,119046
Seq#:37;  N Pos.  119047,119048,119049,119050,119051,119052,119053,119054
Seq#:37;  N Pos.  119055,119056,119057,119058,119059,119060,119061,119062
Seq#:37;  N Pos.  119063,119064,119065,119066,119067,119068,119069,119070
Seq#:37;  N Pos.  119071,119072,119073,119074,119075,119076,119077,119078
Seq#:37;  N Pos.  119079,119080,119081,119082,119083,119084,119085,119086
Seq#:37;  N Pos.  119087,119088,119089,119090,119091,119092,119093,119094
Seq#:37;  N Pos.  119095,119096,119097,119098,119099,119100,119101,119102
Seq#:37;  N Pos.  119103,119104,119105,119106,119107,119108,119109,119110
Seq#:37;  N Pos.  119111,119112,119115,119116,119117,119118,119119,119120
Seq#:37;  N Pos.  119121,119123,141674,142063,142137,142967,143077,143506
Seq#:37;  N Pos.  143587,143629,149079
```

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

```
Seq#:8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32
Seq#:33,34,35,36,39,40,41,42,43,44,45,46,47
```

```
L:1937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:5314
L:2213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:8074
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:10294
L:2427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:14494
L:2455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15334
L:2459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:15454
L:2485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16234
L:2487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16294
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16354
L:3809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:55954
L:3865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:57634
L:3957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:60394
L:3979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:61054
L:5243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:98202
L:5303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:99719
L:5583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:108053
L:5617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:109073
L:5943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118853
L:5947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:118973
L:5949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119033
L:5951 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:119093
L:6725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:141615
L:6739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142035
L:6741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142095
L:6769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:142935
L:6773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143055
L:6787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143475
L:6789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143535
L:6791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:143595
L:6979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:149027
```